

102101 91286860



Docket No.: PF-0181-2 CON
Inventors: Hillman et al.
Title: NOVEL HUMAN MEMBRANE PROTEIN
Serial No.: 09/898,216

#4

9	5' GGC TTC TGG GAG CNA CCG CTC CGC TCG TCT CGT TGG TTC CGG AGG TCG CTG CGG	54
63	CGG TGG GAA ATG CTG GCG CGC GCG GCG GGG CAC TGG GGC CCT TTT GCT GAG	108
	M L A R A A R G H W G P F A E	
117	GGG CTC TCT ACT GGC TTC TGG CCG CGC TCC GGC GCC TCC TCT GGA TTG CCC	162
	G L S T G F W P R S G R A S S G L P	
171	CGA AAC ACC GTG GTA CTG TTC TGC CCG CAG CAG GAG GCC TGG GTG GTG GAG CGA	216
	R N T V V L F V P Q Q E A W V V E R	
225	ATG GGC CGA TTC CAC CGG ATC CTG GAG CCT GGT TTG AAC ATC CTC ATC CCT GTG	270
	M G R F H R I L E P G L N I L I P V	
279	TTA GAC CGG ATC CGA TAT GTG CAG AGT CTC AAG GAA ATT GTC ATC AAC GTG CCT	324
	L D R I R Y V Q S L K E I V I N V P	
333	GAG CAG TCG GCT GTG ACT CTC GAC AAT GTA ACT CTG CAA ATC GAT GGA GTC CTT	378
	E Q S A V T L D N V T L Q I D G V L	

FIGURE 1A

387 TAC CTG CGC ATC ATG GAC CCT TAC AAG GCA AGC TAC GGT GTG GAG GAC CCT GAG 432
 Y L R I M D P Y K A S Y G V E D P E

 441 TAT GCC GTC ACC CAG CTA GCT CAA ACA ACC ATG AGA TCA GAG CTC GGC AAA CTC 486
 Y A V T Q L A Q T T M R S E L G K L

 495 TCT NTG GAC AAA GTC TTC CGG GAA CGG GAG TCC CTG AAT GCC AGC ATT GTG GAT 540
 S X D K V F F R E R E S L N A S I V D

 549 GCC ATC AAC CAA GCT GCT GAC TGC TGG GGT ATC CGC TGC CTN CGT TAT GAG ATC 594
 A I N Q A A D C W G I R C L R Y E I

 603 AAG GAT ATC CAT GTG CCA CCC CGG GTG AAA GAG TCT ATG CAG ATG CAG GTG GAG 648
 K D I H V P P R V K E S M Q M Q V E

 657 GCA GAG CGG CGG AAA CGG GCC ACA GTT CTA GAG TCT GAG GGG ACC CGA GAG TCG 702
 A E R R K R A T V L E S E G T R E S

 711 GCC ATC AAT GTG GCA GAA GGG AAG AAA CAG GCC CAG ATC CTG GCC TCC GAA GCA 756
 A I N V A E G K K Q A Q I L A S E A

FIGURE 1B

765	GAA AAG GCT GAA	774	CAG ATA AAT	783	CAG GCA GCA	792	GGA GAG GCC	801	AGT GCA GTT	810	CTG GCG
	E K A E Q		I N Q		A A A		G E A S		A A V		L A
819	AAG GCC AAG GCT	828	AAA GCT GAA	837	GCT ATT CGA	846	ATC CTG GCT	855	GCT CTG	864	ACA CAA
	K A K A A		K A E A I		R I L		A A A		A L T		Q
873	CAT AAT GGA	882	GCA GCA GCT	891	TCA CTG ACT	900	GTG GCC GAG	909	CAG TAT	918	GTC AGC GCG
	H N G D A		A A A S L		T V A E Q		A E Q Y V		S S A		
927	TTC TCC AAA	936	CTG GCC AAG	945	GAC TCC AAC	954	ACT ATC CTA	963	CTG CCC	972	TCC AAC CCT GGC
	F S K L A		K A K D S		N T I L L		P S N P G				
981	GAT GTC ACC	990	AGC ATG GTG	999	GCT CAG GCC	1008	ATG GGT GTA	1017	TAT GGA	1026	GCC CTC ACC AAA
	D V T S M		V A V A Q		A A M G V		Y G A L T		K		
1035	GCC CCA GTG	1044	CCA GGG ACT	1053	CAC TCA CTC	1062	TCC AGT GGG	1071	AGC AGA	1080	GAT GTC
	A P V P G		T P D S L		S S L S G		S S R D V				
1089	CAG GGT ACA	1098	GAT GCA AGT	1107	GAT GAG GAA	1116	CTT GAT CGA	1125	GTC AAG	1134	ATG AGT TAG
	Q G T D A		S X D E L		D E L D R		V K M S *				

FIGURE 1C

Docket No.: PF-0181-2 CON

Inventors: Hillman et al.

Title: NOVEL HUMAN MEMBRANE PROTEIN

Serial No.: 09/898,216

102101-91286860

1143 TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT 1188
1152
1161
1170
1179

3'

FIGURE 1D

Inventors: Hillman et al.

Title: NOVEL HUMAN MEMBRANE PROTEIN

Serial No.: 09/898,216

Questions **A**re **E**ntire **T**he **S**ystem

1	MLARAARGHWG	--PFAEGLSTGFWRPS	--GR	789094
1	MAEKRRDSE	--A--ORLPDSFKDSP	--SK	GI 31069
1	MNLKTCSLSTH	--SFLQKKNEKHGDN	--EH	GI 1065452
1	MEYGMPECSYDSVFTYA	HYNDLDMGMYGNPARQGMMLGNK	GI 1353669	
1	MQGA	--W	GI 1591514	
1	M	--KNDME	--W	GI 1591514
28	ASS	--GLPR	--NTVVLTF	789094
26	YDT	--GLPGCGWILVAFSFLFTVITF	GI 1310659	
41	YGNFTYTRDYGVMMEDDK	LSAIELLIFCVSFLFVMTMT	GI 1353669	
5	F	--VAGLVFLAVLVI	279701	
9	F	--WLLGIIALFIIWK	--GI 1591514	
41	PISIWM	--VPOQEAWVVERMGRFHR	--LLEPGLNLI	789094
52	PVSIYF	--CMKIKEYERAVIFRLGRILGGAKGPGJFFIL	GI 31069	
81	PLSLF	--ALKFISTSEKLVRLRLGRAQK	--TRGPGITLVI	GI 1065452
18	AIIVAKSVAL	IPQAEAVIEFRLGRVSR	--TVSGQLTTLV	279701
24	---	--AIVINQVEVGGGLFIFRLGRVI	--GKLPKGSINII	GI 1591514
68	PVLDRIYVQSLKEIVINVP	EQSAVTLDNVTLOIDGVLYL	789094	
86	PCTDSF	--IKVDMRTISFDIPPOEILTKDSVTISVDGVVY	GI 31069	
111	PCIESY	--TKVDRTSVFSVPPOEILTKDSVTISVDGVVY	GI 1065452	
91	PCIDTTH	--KVTMSITAFNVPPILITDRGLVELGATVPL	GI 1353669	
56	PFIDRVAR	DLREVRVFSFPQPVITEDNLTLNIDTVVVF	279701	
55	PFLEHVP	--VKVDMRTRVTDIPPOEMI	TKDNVAVVKVDAVVVY	GI 1591514
108	RIMDPYKASGVVEDPEYAV	TOLAQTMRSELGKLSXDKKVP	789094	
125	RQNATLA	VANITNADSTRLLAQTTLRNVLGTKNLSQIL	GI 31069	
130	RISNATSV	SVANVENAHSTRLLAQTTLRNMLGTRLSL	GI 1065452	
157	KLIRP	IIAAVCGVORNASVRLANTMLRYISIKKRICDV	GI 1353669	
96	QTVHQAA	VVEISNYVUGVEQLTQTTLRNVVGGMTLEQL	279701	
94	RVIDVEKA	ILEVEDVEYAINLAQTTLRLAIGGSMLEDEVL	GI 1591514	

FIGURE 2A

148 R - - E R E S L N A S I V D A I N O A A D C W G I R C L R V E I K D I H V P P R 789094
 160 S - - D R E T A H N Q S T I D E A T S W G I K V E R V E I K D V R L P V Q G I 31069
 170 S - - D R E T A A S M Q T I L D E A T S W G I K V E R V E I K D V R L P V Q G I 1065452
 197 S S Q D R R I S A N L K D E L G S F T C Q F G V E I T D V E I S D V K I - - G I 1353669
 136 T - - S R D Q I N A Q L R G V L D E A T C R G W L N V A R V E L R S I D P P S 79701
 134 N - K R E Y I N S K L L E I L D R E T D A W G V R I E K V E V K E I D P E D G I 1591514
 186 V K E S M O M Q V E A E R R K R A T V L E S E G T R E S A I N V A E G K K O A O 789094
 203 L Q R A M A A E A S R E A R A K V I A A E G E M N A - - - - G I 31069
 208 L Q R A M A A E A E A T R E A R A K V I A A E G E O K A - - - - G I 1065452
 234 V K E G E N M G S A - - - - - L S S V A K S D A G Q L W Q G I 1353669
 174 I O A S M E K Q M K A D R E K R A M I L T A E G T R E A A I K O A E G O K O A O 79701
 172 I K N A M A Q Q M K A E R L K R A A I L E A E G E K P E G I 1591514
 226 I L A S E A E K A E Q I N Q A A G E A S A V L A K A K A E A I - - - - - 789094
 231 - - - - - S R A L K E A S M V I T E - - - - - G I 31069
 236 - - - - - S R A L R D A S V I A Q - - - - - G I 1065452
 260 V I G P - - - - - V F E D F A K E C A A E E K A E N A P L V D L - - - - G I 1353669
 214 I L A A E G A R Q A A I L A A E A D R Q S R M L R A Q G E R A A Y L Q A Q Q G 79701
 259 - R I L A A A L T Q H N G D A A S L T V A E Q V S A F S K L A K D S N T I L 789094
 244 - - - - - S P A A L Q L R Y L Q T L T T I A A E K N S T I G I 31069
 249 - - - - - S P A A L Q L R Y L Q T L N S V A R E K - - - - G I 1065452
 288 S D V P S T S A A G T S T I T P N I P S I D H L I S V A S L A M D E H - L V G I 1353669
 254 A K A I E K T P A A I K A G R P T P E M L A Y Q Y L Q T L P E M A R G D A N K V 79701
 298 - - - - - L P S N P G D V T S M V A O A M - - G V Y G A L T K A P V P G T P D 789094
 268 - - - - - V F E L P I D M - - - - - G I 31069
 269 - - - - - F D D H L P T - - - - - G I 1065452
 327 R L I G R V F Q I N C K D I E P - I C I D L K H G S G A Y K G T S L - - N P D G I 1353669
 294 W V V P S D F N A A L Q G T R L L G K G E D G V P - R F E P S P V E D Q P K 79701

FIGURE 2B

1997

10

FIGURE 2C

Library	Lib Description	Abun	Pct	Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703	
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577	
TESTNOT03	testis, 37 M	1	0.0557	
LIVRNOT02	liver, 32 F	1	0.0515	
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418	
LVENNOT03	heart, left ventricle, 31 M	1	0.0336	
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309	
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288	
KERANOT01	keratinocytes, neonatal M	1	0.0227	
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194	
LUNGNOT04	lung, 2 M	1	0.0182	
PGANNOT01	paraganglia, 46 M	1	0.0159	
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150	

FIGURE 3

09898216.101201